

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/511,130
Source: PCP/10
Date Processed by STIC: 9/19/05

ENTERED



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/511,130

DATE: 09/19/2005

TIME: 15:08:40

Input Set : A:\PTO.KD.txt
 Output Set: N:\CRF4\09192005\J511130.raw

3 <110> APPLICANT: The University of Newcastle
 4 Connolly, Bernard
 5 Fogg, Mark
 6 Pearl, Laurence
 8 <120> TITLE OF INVENTION: DNA POLYMERASES
 10 <130> FILE REFERENCE: P89103PWO
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/511,130
 C--> 13 <141> CURRENT FILING DATE: 2004-10-13
 15 <160> NUMBER OF SEQ ID NOS: 32
 17 <170> SOFTWARE: PatentIn version 3.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 776
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Unknown
 24 <220> FEATURE:
 25 <223> OTHER INFORMATION: Variant derived from Pyrococcus furiosus Pfu-Polymerase
 27 <400> SEQUENCE: 1
 29 Met Ala Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val
 30 1 5 10 15
 33 Ile Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp
 34 20 25 30
 37 Arg Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys
 38 35 40 45
 41 Ile Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val
 42 50 55 60
 45 Arg Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro
 46 65 70 75 80
 49 Ile Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr
 50 85 90 95
 53 Ile Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu
 54 100 105 110
 57 Tyr Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile
 58 115 120 125
 61 Pro Met Glu Gly Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu
 62 130 135 140
 65 Thr Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met
 66 145 150 155 160
 69 Ile Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn
 70 165 170 175
 73 Ile Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile
 74 180 185 190
 77 Lys Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val
 78 195 200 205

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81 Thr Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala
82      210          215          220
85 Glu Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro
86 225          230          235          240
89 Lys Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg
90          245          250          255
93 Ile His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro
94          260          265          270
97 Thr Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys
98          275          280          285
101 Glu Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu
102      290          295          300
105 Asn Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr
106 305          310          315          320
109 Tyr Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg
110          325          330          335
113 Leu Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn
114          340          345          350
117 Leu Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val
118          355          360          365
121 Ala Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu
122      370          375          380
125 Ser Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu
126 385          390          395          400
129 Asn Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile
130          405          410          415
133 Thr His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn
134          420          425          430
137 Tyr Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro
138          435          440          445
141 Gly Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys
142          450          455          460
145 Ile Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu
146 465          470          475          480
149 Leu Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr
150          485          490          495
153 Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala
154          500          505          510
157 Glu Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys
158          515          520          525
161 Glu Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp
162          530          535          540
165 Gly Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys
166 545          550          555          560
169 Lys Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu
170          565          570          575
173 Leu Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr
174          580          585          590
177 Lys Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg

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178	595	600	605
181	Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr		
182	610	615	620
185	Gln Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu		
186	625	630	635
189	640		
190	Ala Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu		
193	645	650	655
194	Ile Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu		
197	660	665	670
198	His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu		
201	675	680	685
202	Ala Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile		
205	690	695	700
206	Val Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu		
209	705	710	715
210	720		
213	Glu Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu		
214	725	730	735
217	Asn Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr		
218	740	745	750
221	Arg Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr		
222	755	760	765
225	<210> SEQ ID NO: 2		
226	<211> LENGTH: 775		
227	<212> TYPE: PRT		
228	<213> ORGANISM: Pyrococcus furiosus		
230	<400> SEQUENCE: 2		
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233	1	5	10
236	15		
237	Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg		
240	20	25	30
241	240	245	250
244	Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile		
245	35	40	45
248	Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg		
249	50	55	60
252	248	253	258
253	Glutamate Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile		
256	65	70	75
257	80		
258	Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile		
259	85	90	95
260	256	261	266
261	Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr		
264	100	105	110
265	260	261	267
266	Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro		
267	115	120	125
268	264	265	270
269	Met Glu Gly Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr		
272	130	135	140
272	Leu Tyr His Glu Gly Glu Phe Gly Lys Gly Pro Ile Ile Met Ile		
272	145	150	155
272	Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile		

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PATENT APPLICATION: US/10/511,130

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273	165	170	175
276 Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys			
277	180	185	190
280 Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr			
281	195	200	205
284 Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu			
285	210	215	220
288 Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys			
289	225	230	235
292 Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile			
293	245	250	255
296 His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr			
297	260	265	270
300 Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu			
301	275	280	285
304 Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn			
305	290	295	300
308 Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr			
309	305	310	315
312 Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu			
313	325	330	335
316 Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu			
317	340	345	350
320 Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala			
321	355	360	365
324 Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser			
325	370	375	380
328 Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn			
329	385	390	395
332 Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr			
333	405	410	415
336 His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr			
337	420	425	430
340 Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly			
341	435	440	445
344 Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile			
345	450	455	460
348 Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu Leu			
349	465	470	475
352 Asp Tyr Arg Gln Lys Ala Ile Lys Leu Ala Asn Ser Phe Tyr Gly			
353	485	490	495
356 Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu			
357	500	505	510
360 Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys Glu			
361	515	520	525
364 Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly			
365	530	535	540
368 Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys Lys			
369	545	550	555
			560

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Input Set : A:\PTO.KD.txt

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372 Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
 373 565 570 575
 376 Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
 377 580 585 590
 380 Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg Gly
 381 595 600 605
 384 Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
 385 610 615 620
 388 Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu Ala
 389 625 630 635 640
 392 Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu Ile
 393 645 650 655
 396 Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
 397 660 665 670
 400 Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
 401 675 680 685
 404 Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
 405 690 695 700
 408 Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
 409 705 710 715 720
 412 Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
 413 725 730 735
 416 Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
 417 740 745 750
 420 Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr Ser
 421 755 760 765
 424 Trp Leu Asn Ile Lys Lys Ser
 425 770 775
 428 <210> SEQ ID NO: 3
 429 <211> LENGTH: 776
 430 <212> TYPE: PRT
 431 <213> ORGANISM: Unknown
 433 <220> FEATURE:
 434 <223> OTHER INFORMATION: Variant derived from Pyrococcus furiosus Pfu-Polymerase
 436 <400> SEQUENCE: 3
 438 Met Ala Ile Leu Asp Val Asp Ala Ile Thr Glu Glu Gly Lys Pro Val
 439 1 5 10 15
 442 Ile Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp
 443 20 25 30
 446 Arg Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys
 447 35 40 45
 450 Ile Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val
 451 50 55 60
 454 Arg Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro
 455 65 70 75 80
 458 Ile Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr
 459 85 90 95
 462 Ile Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu
 463 100 105 110

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/511,130

DATE: 09/19/2005

TIME: 15:08:41

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\09192005\J511130.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date